



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* Example: 1610

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.

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STIC-Biotech/ChemLib

171003

From: Hines, Ja-Na
Sent: Tuesday, November 08, 2005 2:38 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search

Good Afternoon,
I would like to request a sequence and interference search
for application 10/043,344. In particular SEQ ID NO:50, 61, 74 and 85.

Thanks so much!!
Ja-Na Hines (76048)
AU:1645
Office: Rem 3B29
Mailbox: Rem 3C18
x20859

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: *11/9/05*
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: *4*
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *Q2P*
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
protein - protein search, using SW model
on: November 9, 2005, 19:01:45 ; **Search time:** 28.9506 Seconds
(without alignments)
116.322 Million cell updates/sec
Title: US-10-043-344-61
Effect score: 186
Sequence: 1 FISGETLLEGGFVGPQEGQELGGKPLAHDKKVLGVFS 35
oring table: BLOSUM62
hypothetical prote
B. subtilis YxH a
outer membrane protein oxidoredu
probable
adenylosuccinate synthase
alpha/beta superfamily
lysine demethylase
lysine demethylase
probable Guanylate kinase
brain-specific angiogenesis protein
B. subtilis YxH a
TldD protein - The outer membrane protein
hypothetical protein
hypothetical protein
hypothetical protein
hypothetical protein
H83794
AF1537
AD3203
T37150
A69355
H97349
S34286
S45583
T42312
JB0299
AE1180
D72312
S69701
C65058
C91032
G85937
30 54.5 29.3 193 2
31 54.5 29.3 367 2
32 54.0 1035 2
33 53.5 28.8 312 2
34 53.5 28.8 337 2
35 53 28.5 265 2
36 52.5 28.2 506 1
37 52.5 28.2 515 1
38 52.5 28.2 1171 2
39 52.5 28.2 1256 2
40 51.5 27.7 367 2
41 51.5 27.7 459 2
42 51.5 27.7 707 1
43 51 27.4 148 2
44 51 27.4 163 2
45 51 27.4 163 2

ALIGNMENTS

minimum DB seq length: 0 maximum DB seq length: 200000000
RESULT 1
S70907
transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB12)
C:*Haemophilus influenzae*

st-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : PIR79;*: 1: pir1;*: 2: pir2;*: 3: pir3;*: Mol. Microbiol. 19, 575-586, 1995. A1: Titration and expression of the Haemophilus influenzae transferrin receptor. A1: Reference number: S70901; MUID:96228706; PMID:8830248 A1: Accession: S70907

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

K. Bodenre, s.h.
Submitted to the BMBL Data Library, September 1994
A Reference number: S73320
A Accession: S73320

NO.	Score	Match length	Length	Sequence	Accession
1	92.5	648	2	S7097	transferrin-bindin
2	159	85.5	625	D64107	bindin

C:Genetics:
A:Gene: *tbp2*
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent
C:Protein: bacterial pathogen transferrin-binding protein; tonB-dependent

```

D6107 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd K1)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #text
C:Sequence revision 18-Aug-1995 #text
C:Change date 09-Jul-2004 #text

```

C; Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kuhn, C.; Gocayne, J.D.; Scott, J.; Shirley, A.; Liu, L.J.; Glodek, A.; Kelley, J.M.; Fuhrmann, J.L.; Fritchman, J.L.; Geohagen, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geohagen, D.M.
D64107
isocitrate dehydrogenase [imp
dehydrogenase [imp
conserved hypothetical
hypothetical protein

H.O. Smith, C.M.; Fraser, K.V.; Small, L.A.; McDonald, C.L.; Gnehm, C.L.; McDaniel, L.A.; Authors: Gnehm, C.L.; Authors: Gnehm, C.L.; McDonald, L.A.; Smith, H.O.

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64107
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-625 <LOO>
A;Cross-references: UNIPROT:P44971; GB:U32780; PIDN: AAC22657.1;
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
P;1-17/Domain: signal sequence #status predicted <SIG>
P;18-625/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match Score 85.5%; Pred. No. 1-2e-13; Indels 0; Gaps 0;
Best Local Similarity 85.7%; Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
C;Genetics:
Qy 1 FTSEGTLEGFFYGPQQELGGKFLAHDKVTLGVFS 35
Db 287 FTREGTLEGFFYGPNGEEELGGKFLADKVKFGVFS 321

RESULT 3
S70909 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB30)
A;Variety: *Haemophilus influenzae*
A;Strain: SB30
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70909; S73322
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830348
A;Accession: S70909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-630 <LOO>
A;Cross-references: UNIPROT:Q48042; EMBL:U15056
A;Experimental source: strain SB30, clone DS-1047-3-3
R;Loosmore, S.M.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448, 'T', 450, 'I', 452-630 <LOW>
A;Cross-references: EMBL:U15056; PIDN:MAC43932.1; PIDN:91223951
A;Experimental source: strain SB30, clone DS-1047-3-3
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
P;1-17/Domain: signal sequence #status predicted <SIG>
P;18-630/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match Score 85.5%; Pred. No. 1-2e-13; Indels 0; Gaps 0;
Best Local Similarity 85.7%; Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
C;Genetics:
Qy 1 FTSEGTLEGFFYGPQQELGGKFLAHDKVTLGVFS 35
Db 290 FTSEGTLEGFFYGPNAEELGGKFLADKVKFGVFS 324

RESULT 4
S70910 transferrin-binding protein 2 precursor - *Haemophilus influenzae* (strain SB32)
C;Species: *Haemophilus influenzae*
A;Variety: strain SB32
C;Accession: S70910; S73323
C;Sequence revision 25-Apr-1997 #text_change 09-Jul-2004
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the *Haemophilus influenzae* transferrin receptor genes

A;Reference number: S70901; MUID:96228706; PMID:8830248
 A;Accession: S70908
 A;Molecule type: DNA
 A;Residues: 1-631 <LOO>
 A;Cross-references: UNIPROT:Q48041; EMBL:U15055
 A;Experimental source: strain SB29, clone DS-1090-3-2
 R;Loosmore, S.M.
 Submitted to the EMBL Data Library, September 1994
 A;Reference number: S73320
 A;Accession: S73321
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: EMBL:U15055; NID:SI223948; PIDN:>
 A;Residues: 1-250, L'-252-349, 'RTDATNN', 357-631 <LOW>
 A;Experimental source: strain SB29, clone DS-1090-3-2
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 P;1-17/Domain: signal sequence #status predicted <SIG>
 P;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match Score 156 ; DB 2; Length 631;
 Best Local Similarity 82.9%; Pred. No. 3.1e-13;
 Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 35
 Db 290 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 324

RESULT 7
 S70004 transferrin-binding protein 2 precursor - Haemophilus influenzae (strains Eagan and Minn)
 C;Species: Haemophilus influenzae
 A;Variety: strains Eagan and strain Minna
 C;Date: 15-Feb-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C;Accession: S70904; S70902
 R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A;Reference number: S70901; MUID:96228706; PMID:8830248
 A;Accession: S70904
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-660 <LOO>
 A;Cross-references: UNIPROT:Q57443; EMBL:U15051; NID:91223307; PIDN: AAC41924.1; PID:91223307
 A;Accession: S70902
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-660 <LO2>
 A;Cross-references: EMBL:U15052; NID:91223302; PIDN: AAC43926.1; PID:91223302
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 P;1-17/Domain: signal sequence #status predicted <SIG>
 P;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match Score 150 ; DB 2; Length 660;
 Best Local Similarity 80.0%; Pred. No. 2.1e-12;
 Matches 28; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 FTSEGTLGGFPYGPQEGLGSKFLAHDKVKLGVSF 35
 Db 288 FTSEGTLGGFPYGPNAEELGSKFLATDNRVFGVFS 322

RESULT 8
 S49815 transferrin-binding protein - Actinobacillus pleuropneumoniae
 C;Species: Actinobacillus pleuropneumoniae
 C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S49815
 R;Bunka, S.; Potter, A.; Gerlach, G.
 submitted to the EMBL Data Library, November 1994
 A;Description: Cloning and sequencing of the transferrin-binding protein genes of Actino
 A;Reference number: S49814
 A;Accession: S49814
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q44167; EMBL:246774; NID:9577526; PIDN:CAA86729.1; PID:9577526
 C;Genetics:
 A;Gene: tiba
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 Query Match Score 109 ; DB 2; Length 547;
 Best Local Similarity 65.5%; Pred. No. 6.6e-07;
 Matches 19; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 7 LEGGYGPEQELGGSKFLAHDKVKLGVSF 35
 Db 273 LEGGYGPKSEELAGKFVAHDKSLEAVFS 301

RESULT 9
 S49814 transferrin-binding protein, outer membrane - Actinobacillus pleuropneumoniae
 C;Species: Actinobacillus pleuropneumoniae
 C;Accession: S49814
 R;Bunka, S.; Potter, A.; Gerlach, G.
 submitted to the EMBL Data Library, November 1994
 A;Description: Cloning and sequencing of the transferrin-binding protein genes of Actino
 A;Reference number: S49814
 A;Accession: S49814
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q44167; EMBL:246774; NID:9577526; PIDN:CAA86729.1; PID:9577526
 C;Genetics:
 A;Gene: tiba
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 Query Match Score 113.5 ; DB 2; Length 599;
 Best Local Similarity 62.9%; Pred. No. 1.8e-07;
 Matches 22; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
 Qy 1 FTSEG-TLGGFYGPQEGLGSKFLAHDKVKLGVSF 34
 Db 308 FTSDSDSLLGGFYGPQEGLGSKFLAHDKVKLGVSF 342

Query Match 57.5% Score 107; DB 2; Length 547;
Best Local Similarity 60.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TLEGGFYGPGQELGGKFLAHDKKVLGVP S 35
Db 271 SLEGGFYGPKAEENACKFVANDKSFLFAVFS 300

RESULT 11
A44796 transferrin-binding protein, tfba - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae* PIDN:AAA21929.1; PMID:9141842
C;Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44796; S27484
R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Potter, A.A.; Willson, P.J.
Infect. Immun. 60, 3253-3261, 1992
A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
A;Content: A44796; MUID:92347999; PMID:1639494
A;Accession: A4205; serotype 7
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-593 <GER>
A;Cross-references: UNIPROT:Q44169; EMBL:MB5275; NID:9141842; PIDN:AAA21929.1; PMID:9141842
A;Note: sequence inconsistent with the nucleotide translation
A;Sequence extracted from NCBI backbone (NCBIN:109735, NCBIPI:109736)
C;Genetics:
A;Gene: tfba
A;Description: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
Query Match 57.5% Score 107; DB 2; Length 547;
Best Local Similarity 60.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TLEGGFYGPGQELGGKFLAHDKKVLGVP S 35
Db 271 SLEGGFYGPKAEENACKFVANDKSFLFAVFS 300

RESULT 12
S27483 transferrin-binding protein - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae* PIDN:AAA21929.1; PMID:9141842
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S27483
R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Potter, A.A.; Wilson, P.
Submitted to the EMBL Data Library, March 1992
A;Description: Characterization of an *Actinobacillus pleuropneumoniae* transferrin-bindin
A;Content: S27483
A;Accession: S27483
A;Molecule type: DNA
A;Residues: 1-593 <GER>
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
Query Match 54.8% Score 102; DB 2; Length 593;
Best Local Similarity 48.6%; Pred. No. 6.5e-06;
Matches 17; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGFFYGPQEGELGGKFLAHDKKVLGVP S 35
Db 312 FTDSNYLEGFFYGPKAEEENACKFVNNKSLFAVFA 346

RESULT 13
B44796 transferrin-binding protein, Tfba - *Actinobacillus pleuropneumoniae*
C;Species: *Actinobacillus pleuropneumoniae* PIDN:AAA21929.1; PMID:9141842
C;Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B44796

R;Gerlach, G.F.; Klashinsky, S.; Anderson, C.; Potter, A.A.; Willson, P.J.
Infect. Immun. 60, 3253-3261, 1992
A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
A;Content: A44796; MUID:92347999; PMID:1639494
A;Accession: B44796

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-593 <GER>
A;Cross-references: UNIPROT:Q44169; GB:M85274; NID:9141840; PIDN:AAA21928.1; PMID:9141841
A;Note: sequence extracted from NCBI backbone (NCBIN:109737, NCBIPI:109738)
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
Query Match 54.8% Score 102; DB 2; Length 593;
Best Local Similarity 48.6%; Pred. No. 6.5e-06;
Matches 17; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGFFYGPQEGELGGKFLAHDKKVLGVP S 35
Db 312 FTDSNYLEGFFYGPKAEEENACKFVNNKSLFAVFA 346

RESULT 14
H81070 lactoferrin-binding protein B NMB1541 [imported] - *Neisseria meningitidis* (strain MC58) serogroup B
C;Species: *Neisseria meningitidis*
C;Accession: H81070 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81070
R;Pettelius, H.; Saunders, N.J.; Heidelberger, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, R.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R.; Vei
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Content: AB1000; MUID:20175755; PMID:10710307
A;Accession: H81070
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-737 <TER>
A;Cross-references: UNIPROT:Q9JYK4; GB:AE002098; NID:97226785; PIDN:AAF41895
C;Genetics:
A;Gene: NMB1541

Query Match 52.2% Score 97; DB 2; Length 737;
Best Local Similarity 55.2%; Pred. No. 3.9e-05;
Matches 16; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 7 LEGFFYGPQEGELGGKFLAHDKKVLGVP S 35
Db 330 LEGFFGDNGLAEGRFSNDNSVGFVPA 358

RESULT 15
D81798 lactoferrin-binding protein NMA1740 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup B
C;Species: *Neisseria meningitidis*
C;Accession: D81798 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, I.; Holroyd, S.; Jolley, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, NATURE 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Content: A81775; MUID:20222556; PMID:10761919
A;Accession: D81798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-741 <PAR>
A;Cross-references: UNIPROT:Q9JYK3; GB:AL162757; NID:97380371; PIDN:CA84966
C;Genetics:
A;Experimental source: serogroup A, strain Z2491
A;Gene: LbpB; NMA1740

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Query Match      52.2%; Score 97; DB:2; Length 741;
Best Local Similarity 55.2%; Pred. No. 3.9e-05;
Matches 16; Conservative 7; Mismatches 6; Indels 0;
Gaps 0;

Qy   7 LEGGPYGPBGOBLGGKPLAHDKKVKGVPES 35
     |||||:|:|||:||:||:|:||:||:||:|
Db  326 LEGGFFGDDNGEBLAGRFISNDNSVFGVFA 354
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Search completed: November 9, 2005, 19:24:01
Job time : 34.9506 sec

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[1]	RN	SEQUENCE FROM N.A.	OS	Neisseria sicca.
	RP		OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
	RC		CC	Neisseriaceae; Neisseria.
	STRAIN=2717;		NCBI_TaxID=49;	
	RX MEDLINE=2407297; PubMed=10948108;		OX	
	RX DOI=10.1128/IAI.68.4.938-4.940; 2000;		RN	
	RA Rokbi B., Renaud-Mongené G., Mignon M., Danve B., Poncet D., Chabane C., Caugant A., Quentin-Millet M.J.;	[1]	RP	SEQUENCE FROM N.A.
	RA "Allelic diversity of the two transferrin binding protein B genes representative of Neisseria meningitidis strains of a collection of Neisseria meningitidis strains of a recombinant TbpB-based vaccine.";	RC STRAIN=9913;	RC	
	RT EMBL; AR279554; AAC055881; -.	RA Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.	RA	
	RL Infect. Immun. 68:938-947 (2000).	DR EMBL; AU704730; CAG28812.2; -.	DR	
	DR GO; GO:0004998; P:transferrin receptor activity; IEA.	DR GO; GO:0004998; P:transferrin receptor activity; IEA.	DR	
	DR InterPro; IPR001677; Transferrin bind.	DR InterPro; IPR001677; Transferrin bind.	DR	
	DR Pfam; PF01298; Lipoprotein_5.	DR Pfam; PF01298; Lipoprotein_5.	DR	
	DR GO; GO:0004998; F:transferrin receptor activity; IEA.	SQ SEQUENCE 593 AA; 64257 MW; 46187C48497275BA CRC64;	SQ	
	DR InterPro; IPR001677; Transferrin bind.	Query Match 77.4%; Score 127; DB 2; Length 593;		
	DR Pfam; PF01298; Lipoprotein_5.	Best Local Similarity 77.4%; Pred. No. 7.1e-09;		
	FT NON_TER 1	Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
	FT CHATN <1	Db 318 LEGGYGPKQDDELGGKFLANDKKVLAFFSAK 348		
	SEQUENCE 582 AA; 63426 MW; 2694AD04F2507F4 CRC64;	RESULT 12		
	Qy 1 LEGGFYGPKEBELGPRFLADDKVPGVFSAK 31	O6HW3 PRELIMINARY; PRT; 594 AA.		
	Db 307 LEGGFYGPQDDELGSKFLANDKKVLAFFSAK 337	ID O6HW3 PRELIMINARY; PRT; 594 AA.		
	RESULT 10	Q6HW5 PRELIMINARY; PRT; 593 AA.		
	ID Q6HW5	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	AC O6HW5; DT 05-JUL-2004 (TREMBLrel. 27, Created)	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DE Transferrin binding protein B.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	GN Name=tbpB;	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	OS Neisseria cinerea.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	OC Neisseriaceae; Neisseria.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	NCBI_TaxID=483;	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	RP SEQUENCE FROM N.A.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	RA "Allelic diversity of the two transferrin binding protein B genes representative of Neisseria meningitidis strains of a recombinant TbpB-based vaccine.";	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B., Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DR EMBL; AU704731; CAG28813.2; -.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DR GO; GO:0016020; C:membrane; IEA.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DR InterPro; IPR001677; Transferrin bind.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	DR Pfam; PF01298; Lipoprotein_5.	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	SQ SEQUENCE 593 AA; 6421.8 MW; 8F67EAB15A9FEA9 CRC64;	AC Q6HW3 PRELIMINARY; PRT; 594 AA.		
	Query Match 77.4%; Score 127; DB 2; Length 594;	Query Match 77.4%; Score 127; DB 2; Length 594;		
	Best Local Similarity 77.4%; Pred. No. 7.1e-09;	Best Local Similarity 77.4%; Pred. No. 7.1e-09;		
	Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
	Db 318 LEGGYGPKQDDELGSKFLANDKKVLAFFSAK 348	Db 318 LEGGYGPKQDDELGSKFLANDKKVLAFFSAK 348		
	RESULT 13	Q6HW6 PRELIMINARY; PRT; 602 AA.		
	ID Q6HW6	AC 053991 PRELIMINARY; PRT; 602 AA.		
	AC 06JBW6; DT 01-JUN-1998 (TREMBLrel. 06, Created)	AC 053991 PRELIMINARY; PRT; 602 AA.		
	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	AC 053991 PRELIMINARY; PRT; 602 AA.		
	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC 053991 PRELIMINARY; PRT; 602 AA.		
	DE TbpB precursor.	AC 053991 PRELIMINARY; PRT; 602 AA.		
	GN Name=tbpB;	AC 053991 PRELIMINARY; PRT; 602 AA.		
	OS Neisseria meningitidis.	AC 053991 PRELIMINARY; PRT; 602 AA.		
	OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	AC 053991 PRELIMINARY; PRT; 602 AA.		
	OC Neisseriaceae; Neisseria.	AC 053991 PRELIMINARY; PRT; 602 AA.		
	NCBI_TaxID=483;	AC 053991 PRELIMINARY; PRT; 602 AA.		
	RN [1]			

RP SEQUENCE FROM N.A.
 RC STRAIN=2713;
 RX MEDLINE=98148004; PubMed=9479046; DOI=10.1016/S0378-1119(97)00646-X;
 RA Legrain M.; Robbi B.; Villevie D.; Jacobs E.;
 RT "Characterization of genetic exchanges between various highly
 divergent tbpB's having occurred in *Neisseria meningitidis*."
 RT
 RL EMBL; AU723044; CAA11047; 1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 KW SIGNAL
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 602 TbpB.
 SQ SEQUENCE 602 AA; 65488 MW; 74641BF77B61C257 CRC64;
 Query Match 77.4%; Score 127; DB 2; Length 602;
 Best Local Similarity 77.4%; Pred. No. 7.2e-0;
 Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Db 327 LEGGPYGPKGEBALGPRFLAGDKKVKVPEVSAK 31
 327 LEGGPYGPQGDBLGKPLANDKKVLAVFSAK 357

RESULT 14
 Q6HBW0 PRELIMINARY; PRT; 594 AA.
 AC Q6HBW0;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DB Transferin binding protein B.
 GN Name=tbpB;
 OS *Neisseria flavescens*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=484;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=414, and 3191;
 RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Robbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AU704736; CAG8818; 2;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004998; P:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5; 1.
 SQ SEQUENCE 594 AA; 64345 MW; 6200B465BP793P20A CRC64;
 Query Match 76.2%; Score 125; DB 2; Length 594;
 Best Local Similarity 77.4%; Pred. No. 1.3e-0;
 Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Db 318 LEGGPYGPQGDBLGKPLANDKKVLAVFSAK 31
 318 LEGGPYGPQGDBLGKPLANDKKVLAVFSAK 348

RESULT 15
 Q6HBW1 PRELIMINARY; PRT; 594 AA.
 AC Q6HBW1;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DB Transferin binding protein B.
 GN Name=tbpB;
 OS *Neisseria flavescens*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.

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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 25.642 Seconds
(without alignments)
116.322 Million cell updates/sec

Title: US-10-043-344-50
Perfect score: 164
Sequence: 1 LEGGFYGPKGRLGFRPLAGDKCKVFGVFSAK 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 962167/63 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing First 45 summaries

PIR 79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	147	89.6	625	2	D64107		transferrin-bindin
2	145	88.4	648	2			transferrin-bindin
3	139	84.8	631	2	S70908		transferrin-bindin
4	135	82.3	630	2	S70909		transferrin-bindin
5	135	82.3	631	2	S70910		transferrin-bindin
6	131	79.9	654	2	S70905		transferrin-bindin
7	125	76.2	660	2	S70904		transferrin-bindin
8	119	72.6	711	2	S70660		transferrin-bindin
9	115	70.1	547	2	S49815		transferrin-bindin
10	115	70.1	547	2	A44796		transferrin-bindin
11	115	70.1	689	2	D81832		transferrin-bindin
12	115	70.1	698	2	D81798		transferrin-bindin
13	114	69.5	599	2	JN0818		transferrin-bindin
14	111	67.7	711	2	JN0820		transferrin-bindin
15	111	67.7	712	2	E81196		transferrin-bindin
16	105	64.0	547	2	S49814		transferrin-bindin
17	104	63.4	737	2	HB1070		lactoferrin-bindin
18	104	63.4	741	2	D81798		lactoferrin-bindin
19	102	62.2	593	2	S27483		transferrin-bindin
20	102	62.2	593	2	B44796		transferrin-bindin
21	66	40.2	488	2	E81003		transferrin-bindin
22	66	40.2	497	2	C82025		probable periplasm
23	62	37.8	289	2	G64105		transferrin-bindin
24	59	36.0	585	2	A83020		probable carboxylic acid sequence not shown
25	57	34.8	742	2	A49341		isocitrate dehydrogenase
26	54	32.9	389	2	T44975		lmp
27	52	32.0	521	2	T27606		hypothetical prote
28	52	31.7	316	2	T19435		hypothetical prote
29	52	31.7	539	2	T28770		hypothetical prote

ALIGNMENTS

RESULT 1
D64107
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64107
/ Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Weidman, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-Genome Random Sequencing and Assembly of Haemophilus influenzae Rd.
A;Accession: D64107
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-625 <TIGR>
A;Cross-references: UNIPROT:P44971; GB:U32780; GB:L42023; NID:91574020; PIDN: AAC22657.1;
C;Genetics:

A;Gene: bpp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-625/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 89.6%; Score 147; DB 2; Length 625;
Best Local Similarity 90.3%; Pred. No. 1..1e-12;
Matches 28; Conservative 1; Missmatches 2; Indels 0; Gaps 0;

Qy 1 LEGGPYGPKGEBELGPRFLAGDKYVGVSXK 31
Db 293 LEGGPYGPNGPSELGGKPLADKRYVGVSXK 323

RESULT 2
S70907
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)
C;Species: Haemophilus influenzae
A;Variety: Strain SB12
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70907; S73320
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Hartness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70907
A;Accession: S70907
A;Molecule type: DNA
A;Residues: 1-648 <LOO>
A;Cross-references: UNIPROT:Q48040; ENZY:U15054
A;Experimental source: strain SB12, clone DS-1047-1-2
R;Loosmore, S.M.
Submitted to the EMBL Data Library, September 1994

A; Reference number: S73320
A; Accession: S73320
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-630 <LOO>
A; Cross-references: EMBL:U15054; NID:gi1223946; PIDN: AAC43930.1; PMID:91223947
A; Experimental source: strain SB12, clone DS-1047-1-2
C; Genetics:
A; Gene: tbp2
C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F; i=17/Domain: signal sequence #status predicted <SIG>
F; i=18-648/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match 88.4%; Score 145; DB 2; Length 648;
Best Local Similarity 87.1%; Pred. No. 2.2e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEGGFYGPKGEBLGFRFLAGDKKVFGVFSAK 31
Db 297 LEGGFYGPGBGEBLGKFLAGDKKVFGVFSAK 327

RESULT 3
S70908 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C; Species: Haemophilus influenzae
A; Variety: strain SB29
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: S70908; S73321
R; Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A; Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A; Reference number: S70901; MUID:96228706; PMID:8830248
A; Accession: S70908
A; Molecule type: DNA
A; Residues: 1-631 <LOO>
A; Cross-references: UNIPROT:Q48041; EMBL:U15055
A; Experimental source: strain SB29, clone DS-1090-3-2
R; Loosmore, S.M.
Submitted to the EMBL Data Library, September 1994
A; Reference number: S73320
A; Accession: S73320
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-250, 'L' 252-349, 'RTDATTN' 357-631 <LOW>
A; Cross-references: EMBL:U15055; NID:gi1223948; PIDN: AAC43931.1; PMID:91223949
A; Experimental source: strain SB29, clone DS-1090-3-2
C; Genetics:
A; Gene: tbp2
C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F; i=17/Domain: signal sequence #status predicted <SIG>
F; i=18-631/Product: transferrin-binding protein 2 #status predicted <MAT>
Query Match 84.8%; Score 139; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 1.5e-11;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBLGFRFLAGDKKVFGVFSAK 31
Db 296 LEGGFYGPGBGEBLGKFLAGDNRYFGVFSAK 326

RESULT 4
S70909 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB30)
C; Species: Haemophilus influenzae
A; Variety: strain SB30
C; Accession: S70909; S73322
R; Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A; Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A; Reference number: S70901; MUID:96228706; PMID:8830248

Query Match 82.3%; Score 135; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 5.5e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LEGGFYGPKGEBLGFRFLAGDKKVFGVFSAK 31
Db 296 LEGGFYGPGBGEBLGKFLASDKKVFGVFSAK 326

RESULT 6
S70905

transferrin-binding protein 2 precursor - Haemophilus influenzae (strain PAK 12085)

C;Accession: S70660
 R;Legrain, M.; Findeli, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, E.
 C;Species: Haemophilus influenzae
 A;Variety: strain PAK 12085
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S70905
 R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A;Reference number: S70901; MUID:96228706; PMID:8830248
 A;Accession: S70905
 A;Status: preliminary; nucleic acid sequence not shown
 A;Cross-references: UNIPROT:Q48038; EMBL:U15053; NID:gi:223943; PIDN: AAC43928.1; PID:9122
 A;Experimental source: strain PAK 12085
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 P;1-17/Domain: signal sequence #status predicted <SIG>
 P;18-654/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 79.9%; Score 131; DB 2; Length 654;
 Best Local Similarity 80.6%; Pred. No. 2.1e-10;
 Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKGEBLGRFLAGDKKVKVGFSAK 31
 Db 296 LEGGFYGPNAEELGGFLANDERKVFGVFSAK 326
 RESULT 9
 S49815
 transferrin-binding protein - Actinobacillus pleuropneumoniae
 C;Species: Actinobacillus pleuropneumoniae
 C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S49815
 R;Bunka, S.; Porter, A.; Gerlach, G.
 submitted to the EMBL Data Library, November 1994
 A;Description: Cloning and sequencing of the transferrin-binding protein genes of Actino
 Mol. Microbiol. 19, 575-586, 1996
 A;Reference number: S70904; S70902
 A;Accession: S70904; S70902
 R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
 Mol. Microbiol. 19, 575-586, 1996
 A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
 A;Reference number: S70901; MUID:96228706; PMID:8830248
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-660 <LOO>
 A;Cross-references: UNIPROT:Q57443; EMBL:U15051; NID:gi:223937; PIDN: AAC43924.1; PID:9122
 A;Experimental source: strain Eagan, clone S-4368-3-3, JB-901-5-3
 A;Accession: S70902
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-660 <LOO>
 A;Cross-references: EMBL:U15052; NID:gi:223940; PIDN: AAC43926.1; PID:91223941
 C;Genetics:
 A;Gene: tbp2
 C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
 P;1-17/Domain: signal sequence #status predicted <SIG>
 P;18-660/Product: transferrin-binding protein 2 #status predicted <MAT>
 Query Match 76.2%; Score 125; DB 2; Length 660;
 Best Local Similarity 77.4%; Pred. No. 1.5e-09;
 Matches 24; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYGPKGEBLGRFLAGDKKVKVGFSAK 31
 Db 294 LEGGFYGPNAEELGGFLANDERKVFGVFSAK 324
 RESULT 8
 S70660
 transferrin-binding protein 2 precursor - Neisseria meningitidis
 C;Species: Neisseria meningitidis
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match Score 115; DB 2; Length 547;
Best Local Similarity 67.7%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBELGFRFLAGDKKVGVFSAK 31
Db 272 LEGGFYGPKAEMAGFVANDKSLPAVESAK 302

RESULT 11

transferrin-binding protein 2 precursor - *Neisseria meningitidis*
C;Species: *Neisseria meningitidis*
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70661; S37262; S70659

R;Legrain, M.
submitted to the EMBL Data Library, August 1995

A;Reference number: S70661
A;Accession: S70661
A;Molecule type: DNA
A;Residues: 1-69 <LEG>
A;Cross-references: UNIPROT:Q51288; EMBL:250732; NID:91177570; PIDN:CAA90599.1; PID:9117
A;Experimental source: strain B283
R;Wilton, J.; Ala'Aldien, D.; Palmer, H.M.; Borriello, S.P.
FEMS Microbiol. Lett. 107, 59-66, 1993

A;Title: Cloning and partial sequence of transferrin-binding protein 2 of *Neisseria meni*
A;Accession: S37626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 25-65 <WIL>
A;Cross-references: EMBL:X75167; NID:9405780; PIDN:CAA53009.1; PID:9405781
R;Legrain, M.; Finslai, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, R.
Mol. Microbiol. 19, 159-169, 1996

A;Title: Molecular characterization of hybrid Tbp2 proteins from *Neisseria meningitidis*.
A;Reference number: S70659; PMID:96419172; PMID:8821945

A;Accession: S70659
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Genes: 21-245, 'D', 247-260, 'D', 262-689 <LEW>
A;Cross-references: EMBL:250732
C;Genetics:

Query Match Score 115; DB 2; Length 689;
Best Local Similarity 74.2%; Pred. No. 3.9e-08;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBELGFRFLAGDKKVGVFSAK 31
Db 312 LSGGFYGPKGEBELGFRFLSDDKVAVVGSAK 342

RESULT 12

transferrin-binding protein B NMA0205 [imported] - *Neisseria meningitidis* (strain Z2491)
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D81832
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, N.; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 40, 505-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Accession: D81832
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-698 <PAR>
A;Cross-references: UNIPROT:O68937; GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAR8524
A;Experimental source: Serogroup A, strain Z2491
C;Genetics:
A;Gene: tbpB; NMA0205
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match Score 115; DB 2; Length 698;
Best Local Similarity 74.2%; Pred. No. 3.9e-08;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBELGFRFLAGDKKVGVFSAK 31
Db 322 LSGGFYGPKGEBELGFRFLSDDKVAVVGSAK 352

RESULT 13

transferrin-binding protein 2 precursor - *Neisseria meningitidis* (strain B16B6)

C;Species: *Neisseria meningitidis*
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: JN0818; PN0633; S33153

R;Legrain, M.; Mazarin, V.; Irwin, S.W.; Bouchon, B.; Quentin-Millet, M.J.; Jacobs, E.; Gene 130, 73-80, 1993

A;Title: Cloning and characterization of *Neisseria meningitidis* genes encoding the trans
FEMS Microbiol. Lett. 107, 59-66, 1993

A;Reference number: JN0818; MUID:933305825; PMID:8344530

A;Accession: JN0818
A;Molecule type: DNA
A;Residues: 1-599
A;Cross-references: UNIPROT:Q06988; EMBL:Z15129;
A;Molecule type: protein
A;Residues: 21-3451-61;158-171;351-361;363-368;378-386;441-456;564-582 <LE1>
C;Genetics:

A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

A;Keywords: iron transport; membrane protein; metal binding
F;1-20/Domain: signal sequence #status predicted <SG>
F;21-599/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match Score 114; DB 2; Length 599;
Best Local Similarity 71.0%; Pred. No. 4.6e-08;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKGEBELGFRFLAGDKKVGVFSAK 31
Db 315 LEGGFYGPKGEBELGAKPLSNDNKKVAVFGAK 345

RESULT 14

transferrin-binding protein 2 precursor - *Neisseria meningitidis* (strain M982)

C;Species: *Neisseria meningitidis*
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: JN0820; PN0635; S33155

R;Legrain, M.; Mazarin, V.; Irwin, S.W.; Bouchon, B.; Quentin-Millet, M.J.; Jacobs, E.; Gene 130, 73-80, 1993

A;Title: Cloning and characterization of *Neisseria meningitidis* genes encoding the trans
FEMS Microbiol. Lett. 107, 59-66, 1993

A;Reference number: JN0818; MUID:933305825; PMID:8344530

A;Accession: JN0820
A;Molecule type: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-711 <LEG>
A;Cross-references: UNIPROT:Q09057; EMBL:Z15130;
A;Accession: PN0635
A;Molecule type: protein
A;Residues: 21-3358-65;144-161;178-190;419-424 <LE1>
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

C;Keywords: iron transport; membrane protein; metal binding

F;1-20/Domain: signal sequence #status predicted <SIG>
 P;21-71/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 67.7%; Score 111; DB 2; Length 711;
 Best Local Similarity 71.0%; Pred. No. 1.5e-07;
 Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYCPKGBELGFRFLAGDKRKFVFGVFSAK 31
 Db 335 LSGGFPGPQGBELGFRPLSDDKAVVGSAK 365

RESULT 15

E81196 transferrin-binding protein 2 NMB0460 [Imported] - Neisseria meningitidis (strain MC58) 6
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: E81196
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.
 Hickie, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; ve
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; PMID:20175755; PMID:10710307
 A;Accession: E81196
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-712 <TEST>
 A;Cross references: UNIPROT:Q9KOVO; GB:AE002402; GB:AE002098; NID:g7225683; PIDN:AAF4089
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0460
 C;Superfamily: bacterial pathogen transfrinin-binding protein; tonB-dependent receptor a
 Query Match 67.7%; Score 111; DB 2; Length 712;
 Best Local Similarity 71.0%; Pred. No. 1.5e-07;
 Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 LEGGFYCPKGBELGFRFLAGDKRKFVFGVFSAK 31
 Db 336 LSGGFPGPQGBELGFRPLSDDKAVVGSAK 366

Search completed: November 9, 2005, 19:23:55
 Job time : 26.642 secs

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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:37:18 ; Search time 132.802 Seconds
 (without alignments)

97.669 Million cell updates/sec

Title: US-10-043-344-50

Perfect score: 164

Sequence: LEGGPYGPKGBELGFLERFLAGDKKVGFSAK 31

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
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 2: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB.pep:
 3: /cgn2_6/podata/1/pubpaas/US06_NEWPUB.pep:
 4: /cgn2_6/podata/1/pubpaas/US07_NEWPUB.pep:
 5: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB.pep:
 6: /cgn2_6/podata/1/pubpaas/US07_PCTIG_PUBCOMB.pep:
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 11: /cgn2_6/podata/1/pubpaas/US09_PUBCOMB.pep:
 12: /cgn2_6/podata/1/pubpaas/US09_NEWPUB.pep:
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 14: /cgn2_6/podata/1/pubpaas/US10B_PUBCOMB.pep:
 15: /cgn2_6/podata/1/pubpaas/US10C_PUBCOMB.pep:
 16: /cgn2_6/podata/1/pubpaas/US10B_PUBCOMB.pep:
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 20: /cgn2_6/podata/1/pubpaas/US11_NEWPUB.pep:
 21: /cgn2_6/podata/1/pubpaas/US60_NEWPUB.pep:
 22: /cgn2_6/podata/1/pubpaas/US60_PUBCOMB.pep:
 RESULT 1
 US-10-043-344-50
 / Sequence 50, Application US/10043344
 / Publication No. US2003008886A1
 / GENERAL INFORMATION:
 / APPLICANT: Loosmore, Sheena M.
 / INVENTOR: Hartness, Robbin E.
 / APPLICANT: Schuyvers, Anthony B.
 / APPLICANT: Chong, Pele
 / APPLICANT: Gray-Owen, Scott
 / APPLICANT: Murdin, Andrew D.
 / APPLICANT: Klein, Michel H.
 / TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 / FILE REFERENCE: 1038-1221 MIS
 / CURRENT APPLICATION NUMBER: US/10/043,344
 / PRIOR APPLICATION NUMBER: 08/649,518
 / PRIOR FILING DATE: 1996-05-17
 / NUMBER OF SEQ ID NOS: 160
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 50
 / LENGTH: 31
 / ORGANISM: Haemophilus influenzae
 / TYPE: PRT
 / US-10-043-344-50

Query Match Length DB ID Description

1 164 100.0 31 14 US-10-043-344-50 Sequence 50, Appl

2 145 88.4 648 14 US-10-043-344-109 Sequence 109, Appl

3 139 84.8 631 14 US-10-043-344-111 Sequence 111, Appl

4 135 82.3 630 14 US-10-043-344-113 Sequence 113, Appl

5 135 82.3 631 14 US-10-043-344-115 Sequence 115, Appl

6 131 79.9 644 14 US-10-043-344-6 Sequence 6, Appl

7 131 79.9 654 14 US-10-043-344-12 Sequence 12, Appl

8 125 76.2 365 14 US-10-043-344-156 Sequence 156, Appl

9 125 76.2 404 14 US-10-043-344-155 Sequence 155, Appl

10 125 76.2 411 14 US-10-043-344-154 Sequence 154, Appl

11 125 76.2 417 14 US-10-043-344-153 Sequence 153, Appl

SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	31	14	US-10-043-344-50
2	145	88.4	648	14	US-10-043-344-109
3	139	84.8	631	14	US-10-043-344-111
4	135	82.3	630	14	US-10-043-344-113
5	135	82.3	631	14	US-10-043-344-115
6	131	79.9	644	14	US-10-043-344-6
7	131	79.9	654	14	US-10-043-344-12
8	125	76.2	365	14	US-10-043-344-156
9	125	76.2	404	14	US-10-043-344-155
10	125	76.2	411	14	US-10-043-344-154
11	125	76.2	417	14	US-10-043-344-153

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Qy 1 LEGGYGPKEEBLGPRFLAGDKKVGFSAK 31
 Db 1 LEGGYGPKEEBLGPRFLAGDKKVGFSAK 31

RESULT 2
US-10-043-344-109
Sequence 109, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Harkness, Robin E.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew D.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR FILING DATE: 1996-05-17
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 109
LENGTH: 648
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-043-344-109

Query Match 88.4%; Score 145; DB 14; Length 648;
Best Local Similarity 87.1%; Pred. No. 1.e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 31
Db 297 LEGGGYGPKEBELGSKFLAGDKKVFGVFSAK 327

RESULT 5
US-10-043-344-115
Sequence 115, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Harkness, Robin E.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew D.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/649,518
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 115
LENGTH: 630
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-043-344-115

Query Match 82.3%; Score 135; DB 14; Length 630;
Best Local Similarity 83.9%; Pred. No. 3.e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGYGPKEBELGPRFLAGDKKVFGVFSAK 31
Db 296 LEGGGYGPNAEELGSKFLASDKKVFGVFSAK 326

RESULT 6
US-10-043-344-6
Sequence 6, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 6
 LENGTH: 644
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-6

Query Match 79.9%; Score 131; DB 14; Length 644;
 Best Local Similarity 80.6%; Pred. No. 1.3e-10;
 Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 31
 Db 294 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 324

RESULT 7
 US-10-043-344-12
 / Sequence 12, Application US/10043344
 / Publication No. US20030088086A1
 / GENERAL INFORMATION:
 / APPLICANT: Loosmore, Sheena M.
 / APPLICANT: Harkness, Robin E.
 / APPLICANT: Schryvers, Anthony B.
 / APPLICANT: Chong, Pele
 / APPLICANT: Gray-Owen, Scott
 / APPLICANT: Murdin, Andrew D.
 / APPLICANT: Klein, Michel H.
 / TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 / FILE REFERENCE: 1038-1221 MIS
 / CURRENT APPLICATION NUMBER: US/10/043,344
 / CURRENT FILING DATE: 2002-07-01
 / PRIOR APPLICATION NUMBER: 08/649,518
 / PRIOR FILING DATE: 1996-05-17
 / NUMBER OF SEQ ID NOS: 160
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 12
 / LENGTH: 654
 / TYPE: PRT
 / ORGANISM: Haemophilus influenzae
 US-10-043-344-12

Query Match 79.9%; Score 131; DB 14; Length 654;
 Best Local Similarity 80.6%; Pred. No. 1.3e-10;
 Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 31
 Db 296 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 326

RESULT 10
 US-10-043-344-156
 / Sequence 156, Application US/10043344
 / Publication No. US20030088086A1
 / GENERAL INFORMATION:
 / APPLICANT: Loosmore, Sheena M.
 / APPLICANT: Harkness, Robin E.
 / APPLICANT: Schryvers, Anthony B.
 / APPLICANT: Chong, Pele
 / APPLICANT: Gray-Owen, Scott
 / APPLICANT: Murdin, Andrew D.

Query Match 76.2%; Score 125; DB 14; Length 404;
 Best Local Similarity 77.4%; Pred. No. 5.5e-10;
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 31
 Db 294 LEGGGFVGPKGBELGPRFLAGDKKVGVFSAK 324

RESULT 154
 US-10-043-344-156
 / Sequence 154, Application US/10043344
 / Publication No. US20030088086A1
 / GENERAL INFORMATION:
 / APPLICANT: Loosmore, Sheena M.
 / APPLICANT: Harkness, Robin E.
 / APPLICANT: Schryvers, Anthony B.
 / APPLICANT: Chong, Pele
 / APPLICANT: Gray-Owen, Scott
 / APPLICANT: Murdin, Andrew D.

APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 154
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-50

Query Match 76.2%; Score 125; DB 14; Length 411;
 Best Local Similarity 77.4%; Pred. No. 6.3e-10;
 Matches 24; Conservative 2; N mismatches 5;
 Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGPRFLAGDKKVYGVFSAK 31
 Db 294 LEGGFYGPNAEELGGKFLATDNRVFGVFSAK 324

RESULT 11
 US-10-043-344-153
 Sequence 153, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518
 PRIOR FILING DATE: 1996-05-17
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 153
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-10-043-344-153

Query Match 76.2%; Score 125; DB 14; Length 417;
 Best Local Similarity 77.4%; Pred. No. 6.4e-10;
 Matches 24; Conservative 2; N mismatches 5;
 Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGPRFLAGDKKVYGVFSAK 31
 Db 294 LEGGFYGPNAEELGGKFLATDNRVFGVFSAK 324

RESULT 12
 US-10-043-344-152
 Sequence 152, Application US/10043344
 Publication No. US20030088086A1
 GENERAL INFORMATION:
 APPLICANT: Loosmore, Sheena M.
 APPLICANT: Harkness, Robin E.
 APPLICANT: Schryvers, Anthony B.
 APPLICANT: Chong, Pele
 APPLICANT: Gray-Owen, Scott
 APPLICANT: Murdin, Andrew D.
 APPLICANT: Klein, Michel H.
 TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
 FILE REFERENCE: 1038-1221 MIS
 CURRENT APPLICATION NUMBER: US/10/043,344
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: 08/649,518

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; PRIORITY FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 150
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-150

Query Match      76.2%; Score 125; DB 14; Length 529;
Best Local Similarity 77.4%; Pred. No. 8.3e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy          1 LEGGGPCKGEBLGPFLAGDKKVFGVFSAK 31
Db          294 LEGGGPCKGPNAAEELGKPLATDNRVFGVFSAK 324

RESULT 15
US-10-043-344-149
; Sequence 149, Application US/10043344
; Publication No. US2003008806A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 149
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-149

Query Match      76.2%; Score 125; DB 14; Length 547;
Best Local Similarity 77.4%; Pred. No. 8.6e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy          1 LEGGGPCKGEBLGPFLAGDKKVFGVFSAK 31
Db          294 LEGGGPCKGPNAAEELGKPLATDNRVFGVFSAK 324

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RA	Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M., Harkness R.B., Pele S.c., Klein M.H.; "Cloning and expression of the Haemophilus influenzae transferrin receptor genes.", MBL, EMBL, U15054; AAC4930.1; -.	FT CHAIN 18 625 Probable transferrin-binding protein 2. FT LIPID 18 18 N-Balmitoyl cysteine (Probable). FT LIPID 18 18 S-diacylglycerol Cysteine (Probable). SQ SEQUENCE 625 AA; 69031 MW; 52BFBCT7B5ED4B9A CRC64;
DR	PIR; S70907; S70907.	Query Match 85.5%; Score 159; DB 1; Length 625; Best Local Similarity 85.7%; Pred. No. 5.6e-13; Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
DR	GO; GO:001620; C:membrane; IEA.	Qy 1 FTSEGTLGGFYGPQQELGGKFLAHDKVYLGVFS 35 Db 287 FTSEGTLGGFYGPQQELGGKFLAHDKVYLGVFS 321
DR	InterPro; IPR001677; Transferrin receptor activity; IEA.	
DR	Pfam; PF01298; Lipoprotein_5;	
SQ	SEQUENCE 648 AA; 71246 MW; D89690AE33891A5A CRC64;	
Query Match 92.5%; Score 172; DB 2; Best Local Similarity 94.3%; Pred. No. 9.7e-15; Length 648; Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	RESULT 4 Q48042 PRELIMINARY; PRT; 630 AA. ID Q48042; AC Q48042; DT 01-NOV-1996 (TREMBLrel. 01, Created) AC Q48042; DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) RC STRAIN=SB30; RN [1] RP SEQUENCE FROM N.A. RC MEDLINE=96228706; PubMed=8830248; RN Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M., Harkness R.E., Pele S.c., Klein M.H.; "Cloning and expression of the Haemophilus influenzae transferrin receptor genes.", Mol. Microbiol. 19:575-586(1996). RL EMBL; U15056; AAC43932.1; -. DR PIR; S70909; S70909. DR GO; GO:0016020; C:membrane; IEA. DR GO; GO:0004998; F:transferrin receptor activity; IEA. DR InterPro; IPR01677; Transferrin bind. DR Pfam; PF01298; Lipoprotein_5; 1. SQ SEQUENCE 630 AA; 63573 MW; 6FCB2D1B6B642C84 CRC64;	
Query Match 85.5%; Score 159; DB 2; Length 630; Best Local Similarity 85.7%; Pred. No. 5.6e-13; Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	Qy 1 FTSEGTLGGFYGPQQELGGKFLAHDKVYLGVFS 35 Db 290 FTSEGTLGGFYGPQQELGGKFLAHDKVYLGVFS 324	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.	RESULT 5 Q48043 PRELIMINARY; PRT; 631 AA. ID Q48043; AC Q48043; DT 01-NOV-1996 (TREMBLrel. 01, Created) AC Q48043; DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) RC STRAIN=SB32; RN [1] RP SEQUENCE FROM N.A. OC Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;		
RN	SEQUENCE FROM N.A. STRAIN=Rd / KMP20 / ATCC 51907; MEDLINE=95350630; PubMed=7512800;	
RC	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M., McKinney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodck A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg B., Cottrell M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Grahm C.I., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512(1995).	
RL	- I - FUNCTION: Acts as a transferrin receptor and is required for transferrin utilization (By similarity). - I - SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	CC - I - FUNCTION: Acts as a transferrin receptor and is required for transferrin utilization (By similarity). CC - I - SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	CC DR EMBL; U322780; AAC22657.1; -. DR PIR; D64107; D64107. DR InterPro; IPR001677; Transferrin_bind DR Pfam; PF01298; Lipoprotein_1. DR PROSITE; PS00013; PROKAR_LIPOPROTEIN_1. KW Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor; Signal.	
CC	CC SIGNAL 1 17 Potential.	

OS Neisseria meningitidis.	AC Q6H8W5;	DT 05-JUL-2004	(TREMBLrel. 27, Created)
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)	
OC Neisseriaceae; Neisseria.	DT 05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
NCBI_TaxID=487;	DT 05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
[1]			
RP SEQUENCE FROM N.A.			
STRAIN=Alpha261;			
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;			
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			
DR EMBL: AU04752; CAG28834.1; -.			
DR GO: GO:0016020; C:membrane; IEA.			
DR GO:0004998; F:transferrin receptor activity; IEA.			
DR InterPro: IPR001677; Transferrin_bind.			
DR Pfam: PF01298; Lipoprotein_5'; 1.			
FT NON_TER 1 1			
FT NON_TER 566 566			
SEQUENCE 566 AA; 61751 MW; B0FCA9B682412D8 CRC64;			
Qy 1 FTSEG-TLEGGFYGPEGQBLGGKPLANDKKVLYGFS 35			
Query Match 73.4%; Score 136.5; DB 2; Length 566;			
Best Local Similarity 75.0%; Pred. No. 6e-10;			
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			
Db 284 FVSDSDSLEGGFYGPEGQBLGGKPLANDKKVLYAVFS 319			
RESULT 10			
Q9FC53 PRELIMINARY; PRT; 582 AA.			
AC Q9FC53;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE Transferin binding protein B (Fragment).			
GN Name=tbpB;			
OS Neisseria meningitidis (serogroup B).			
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC Neisseriaceae; Neisseria.			
NCBI_TaxID=491;			
[1]			
RP SEQUENCE FROM N.A.			
STRAIN=204072297; PubMed=10948108;			
DOI=10.118/jai.6.9.4938-4947.2000;			
RA Rokbi B., Renaud Mongeon G., Mignon M., Danve B., Poncelet D., Chabaneil C., Caugant D.A., Quentin-Millet M.J.,			
RT "Allelic diversity of the two transferrin binding protein B gene isotypes among a collection of Neisseria meningitidis strains representative of serogroup B disease: implication for the composition of a recombinant TbpB-based vaccine.";			
RT Infect. Immun. 68:4938-4947 (2000).			
EMBL: AU279554; CMC05588; 1.			
DR GO: GO:016020; C:membrane; IEA.			
GO: GO:004998; F:transferrin receptor activity; IEA.			
DR InterPro: IPR001677; Transferrin_bind.			
DR Pfam: PF01298; Lipoprotein_5'; 1.			
FT CHAIN <1 1 transferrin binding protein B.			
FT CHAIN <1 582 AA; 65426 MW; 26A94AD04P2507F4 CRC64;			
SEQUENCE 582 AA; 73.4%; Score 136.5; DB 2; Length 582;			
Best Local Similarity 75.0%; Pred. No. 6.2e-10;			
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			
Qy 1 FTSEG-TLEGGFYGPEGQBLGGKPLANDKKVLYGFS 35			
Query Match 73.4%; Score 136.5; DB 2; Length 582;			
Best Local Similarity 75.0%; Pred. No. 6.3e-10;			
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			
Db 300 FVSDSDSLEGGFYGPEGQBLGGKPLANDKKVLYAVFS 335			
RESULT 13			
Q6H8W3 PRELIMINARY; PRT; 594 AA.			
AC Q6H8W3;			
DT 03-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DB Transferrin binding protein B.			

GN Name=tbpB;
 OS Neisseria flavescens.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 NCBI_TaxID=484;
 RN [1] _TaxID=484;
 RP SEQUENCE FROM N.A.
 RC STRAIN=13120;
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
 RL EMBL; AJ704733; CAG28815; 2;
 DR GO:0016020; C:membrane; IEA.
 DR GO:004998; F:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5_1.
 SQ SSEQUENCE 594 AA; 64390 MW; P096DB983B046D0B CRC64;
 Query Match 73.4%; Score 136.5; DB 2; Length 594;
 Best Local Similarity 75.0%; Pred. No. 6.3e-10;
 Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 FTSEG-TLEGPFYGPQBLGGKPLAHDKKVLYGVS 35
 Db 311 FVSDSDSLEGGPFYGPQDLGGKFLANDKKVLYAVFS 346

RESULT 14

053391 PRELIMINARY; PRT; 602 AA.
 AC 053391;
 DT 01-JUN-1998 (TREMBurel. 06, Created)
 DT 01-JUN-1998 (TREMBurel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBurel. 24, Last annotation update)
 DB TbpB precursor.
 GN Name=tbpB;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2713;
 RX MEDLINE=98148004; PubMed=9479046; DOI=10.1016/S0378-1119(97)00646-X;
 RA Legrain M.; Robki B.; Villeval D.; Jacobs E.;
 RT "Characterization of genetic exchanges between various highly
 divergent tbps, having occurred in Neisseria meningitidis.";
 RL Gene 20:851-59 (1998).
 DR EMBL; AP223044; CAI11047.1.
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004998; F:transferrin receptor activity; IEA.
 DR InterPro; IPR001677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5_1.
 KW Signal.
 PT SIGNAL 1 20 Potential.
 SQ SSEQUENCE 602 AA; 65488 MW; 74641BP77B61C257 CRC64;
 Query Match 73.4%; Score 136.5; DB 2; Length 602;
 Best Local Similarity 75.0%; Pred. No. 6.4e-10;
 Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 FTSEG-TLEGPFYGPQBLGGKPLAHDKKVLYGVS 35
 Db 320 FVSDSDSLEGGPFYGPQDLGGKFLANDKKVLYAVFS 355

RESULT 15

Q6H8W0 PRELIMINARY; PRT; 594 AA.
 ID Q6H8W0
 AC Q6H8W0;
 DT 05-OCT-2004 (TREMBurel. 27, Created)
 DT 05-OCT-2004 (TREMBurel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBurel. 28, Last annotation update)

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Scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext:				
Searched:	1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl:				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
-	-	-	-	-	-
1	47	100.0	60	2 Q6DKQ8	Q6dkq8 neisseria m
2	47	100.0	410	2 Q6HB8U3	Q6hb8u3 neisseria m
3	47	100.0	526	2 Q71R42	Q71r42 haemophilus
4	47	100.0	545	2 Q71R38	Q71r38 haemophilus
5	47	100.0	547	2 Q44124	Q44124 actinobacil
6	47	100.0	547	2 Q44168	Q44168 actinobacil
7	47	100.0	547	2 Q44170	Q44170 actinobacil
8	47	100.0	560	2 Q71R40	Q71r40 haemophilus
9	47	100.0	566	2 Q6HB8U4	Q6hb8u4 neisseria m
10	47	100.0	567	2 Q6HB8U0	Q6hb8u0 neisseria m
11	47	100.0	569	2 Q6HB8T9	Q6hb8t9 neisseria m
12	47	100.0	569	2 Q6HB8U2	Q6hb8u2 neisseria m
13	47	100.0	570	2 Q6HB8U1	Q6hb8u1 neisseria m
14	47	100.0	571	2 Q6HB8U6	Q6hb8u6 neisseria m
15	47	100.0	572	2 Q6HB8U6	Q6hb8t6 neisseria m
16	47	100.0	573	2 Q6HB8T7	Q6hb8t7 neisseria m
17	47	100.0	579	2 Q9FCS1	Q9fc81 neisseria m
18	47	100.0	579	2 Q9FCS3	Q9fc83 neisseria m
19	47	100.0	582	2 Q9RDV1	Q9rdv1 neisseria m
20	47	100.0	586	2 Q44169	Q44169 actinobacil
21	47	100.0	593	2 Q6HB8V1	Q6hb8v1 neisseria s
22	47	100.0	593	2 Q6HB8W4	Q6hb8w4 neisseria f
23	47	100.0	593	2 Q6HB8W5	Q6hb8w5 neisseria c
24	47	100.0	593	2 Q6HB8W6	Q6hb8w6 neisseria s
25	47	100.0	593	2 Q6HB8V8	Q6hb8v8 neisseria m
26	47	100.0	594	2 Q6HB8W0	Q6hb8w0 neisseria f
27	47	100.0	594	2 Q6HB8V0	Q6hb8v0 neisseria f
28	47	100.0	594	2 Q6HB8W3	Q6hb8w3 neisseria f
29	47	100.0	594	2 Q71R44	Q71r44 actinobacil
30	47	100.0	596	2 Q83UA7	Q83ua7 actinobacil
31	47	100.0	596	2 Q83UA7	Q83ua7 actinobacil

ALIGNMENTS

RESULT 1		PRT;	
ID	Q6DKQ8	PRELIMINARY;	
AC	Q6DKQ8;		
DT	25-OCT-2004 (T-EMBLrel. 28, Created)		
DR	25-OCT-2004 (T-EMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)		
DB	Transferin binding protein B (Fragment).		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
RN	[1] - TAXID=487;		
RP	SEQUENCE FROM N.A.		
RA	Trivedi S.;		
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY660951; AATP13251; -.		
DR	InterPro; IPR001677; Transferrin_bind.		
DR	PFam: PF01298; Lipoprotein_5; 1.		
FT	NON_TER 1		
FT	NON_TER 60 AA; 6509 MW;		
SQ	SEQUENCE 60 AA; 6509 MW; 5A7424D75DFADCP4 CRC64;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
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8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
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8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
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Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
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8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
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Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred. No. 0.47;		
Matches	Mismatches 0; Mismatches 0; Indels 0;		
8	Conservative 0; GapS 0;		
FT	SEQUENCE 60 AA; 6509 MW;		
Query	Match 100.0%; Score 47; DB 2;		
Best	Local Similarity 100.0%; Pred		

Db	272 LEGGFYGP 279	RESULT 7	Q44170	PRELIMINARY;	PRT;	547 AA.						
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			AC Q44170;									
			DT 01-NOV-1996 (TREMBLrel. 01; Created)									
			DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)									
			DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)									
			DE Transferrin-binding protein.									
			GN Name=tfbB;									
			OS Bacterium: Proteobacteria; Gammaproteobacteria; Neisseriales;									
			OC Bacterium: Pasteurellales; Actinomycetales;									
			OC Pasteurellaceae; Actinomycetaceae;									
			RN [1] NCBI_TAXID=715;									
			RP SEQUENCE FROM N.A.									
			RC Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;									
			RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.									
			RC STRAIN=serotype 7;									
			RC MEDLINE=92347999; PubMed=1639494;									
			RA Gerlach G.P.; Klaushinsky S.; Anderson C.; Potter A.A.; Wilson P.J.;									
			RT "Characterization of two genes encoding distinct transferrin-binding proteins in different <i>Actinobacillus pleuropneumoniae</i> isolates.";									
			RL <i>Infect. Immun.</i> 60:3223-3221 (1992).									
			DR PIR: A44796; AA21929.1; -.									
			DR GO: 0016020; C:membrane; IEA.									
			DR GO; GO:000998; F:transferrin receptor activity; IEA.									
			DR InterPro: IPR001677; Transferrin_bind.									
			DR Pfam: PF01298; Lipoprotein_5; 1.									
			SQ SEQUENCE 547 AA; 59849 MW; C3C870FF5867630F CRC64;									
Qy	1 LEGGFYGP 8	Query Match	100.0%; Score 47; DB 2; Length 547;									
			Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps 0;									
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RESULT 8	Q71R40	PRELIMINARY;										
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	AC Q71R40;											
	DT 05-JUL-2004 (TREMBLrel. 27; Created)											
	DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)											
	DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)											
	DB Transferrin binding protein B.											
	GN Name=tbpB;											
	OS Haemophilus parvus.											
	OC Pasteurellales; Gammaproteobacteria; Pasteurellales;											
	OC Pasteurellaceae; Haemophilus.											
	RN [1] NCBI_TAXID=718;											
	RP SEQUENCE FROM N.A.											
	RC STRAIN=H410;											
	RA Ladron N., de la Puent V., Ferri B.P.R., Navas J.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.											
	DR AP376775; AAQ02786.1; -.											
	DR GO; GO:0016020; C:membrane; IEA.											
	DR GO; GO:0004998; F:transferrin receptor activity; IEA.											
	SQ SEQUENCE 560 AA; 61713 MW; 0914C717B69007DC CRC64;											
Qy	1 LEGGFYGP 8	Query Match	100.0%; Score 47; DB 2; Length 560;									
			Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;									
Db	288 LEGGFYGP 295											

RESULT 11

Q6H8U6 PRELIMINARY; PRT; 572 AA.
 ID Q6H8U6
 AC Q6H8U6;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DB Transferrin binding protein B (Fragment).
 GN Name=bpB;
 OS *Neisseria meningitidis*
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Alpha17;
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maidens M., Rokbi B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ704750; CAG28832.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.
 DR InterPro; IPR01677; Transferrin_bind.
 DR Pfam; PF01298; Lipoprotein_5_1.
 FT NON-TER 1 1
 PT NON-TER 572 572
 SQ SEQUENCE 572 AA; 62540 MW; 049BFAD043ACBDOA CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 572;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEGGFTGP 8
Db	292 LEGGFTGP 299

Search completed: November 9, 2005, 19:16:35
 Job time : 33.4938 secs

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OM protein - protein search, using SW model

Run on: November 9, 2005, 18:43:14 ; Search time 31.6296 Seconds
(without alignments)

85.595 Million cell updates/sec

Title: US-10-043-344-85

Perfect score: 40

Sequence: 1 LEGGYFG 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105632 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : A_Geneseq_1.6pc04:*

- 1: geneseqD19808:*
- 2: geneseqD19808:*
- 3: geneseqD20008:*
- 4: geneseqD20018:*
- 5: geneseqD20028:*
- 6: geneseqD20038:*
- 7: geneseqD20038:*
- 8: geneseqD20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AAR77969

ID AAR77969 standard; peptide; 7 AA.

AC	AAR77969;
XX	
DT	09-OCT-1996 (first entry)
XX	
DS	Antigenic Tbp2 peptide TBP2-36.
XX	
KW	Tbp1; Tbp2; transferrin receptor Operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis.
XX	
OS	Synthetic.
XX	
PN	W09513370-A1.
XX	
PD	18-MAY-1995.
XX	
PP	07-NOV-1994; 94WO-CA000616.
XX	
PR	08-NOV-1993; 93US-00148968.
XX	
PR	29-DEC-1993; 93US-00175116.
XX	
PA	(CONN-) CONNAUGHT LAB LTD.
XX	
PI	Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
PI	Yang Y, Mordin A, Klein M;
XX	
DR	WPI: 1995-194099/25.
XX	
PT	Nucleic acids encoding Haemophilus transferin receptor - used to develop PT prods for detection and in diagnosis, prevention and treatment of Haemophilus infection.
XX	
PS	Claim 11; Page 73; 231pp; English.
XX	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	AAR77969	AAR77969 Antigenic
2	40	100.0	7	AAR46162	AAR46162 Predicted
3	40	100.0	7	AAV51767	AAV51767 H. influe
4	40	100.0	7	AAV54121	Aav54121 Tbp2 anti
5	40	100.0	7	AAV89426	Aav89426 Moraxella
6	40	100.0	7	AAV80464	Aav80464 H. influe
7	40	100.0	8	AAR77958	Aar77958 Antigenic
8	40	100.0	8	AAV46151	Aav46151 Predicted
9	40	100.0	8	AAV51756	AAV51756 H. influe
10	40	100.0	8	AAV54110	Aav54110 Tbp2 anti
11	40	100.0	8	AAV80453	Aav80453 H. influe
12	40	100.0	15	AAB77974	Aar77974 H. influe
13	40	100.0	15	AAV51789	Aav51789 H. influe
14	40	100.0	15	AAV54133	Aav54133 Polioviru
15	40	100.0	15	AAV80391	Aav80391 H. influe
16	40	100.0	16	AAR77973	Aar77973 H. influe
17	40	100.0	16	AAV51787	Aav51787 H. influe
18	40	100.0	16	AAV51788	Aav51788 H. influe
19	40	100.0	16	AAV54132	Aav54132 Polioviru
20	40	100.0	16	AAV54131	Aav54131 Polioviru
21	40	100.0	16	AAV80390	Aav80390 H. influe
22	40	100.0	16	AAV80389	Aav80389 H. influe
23	40	100.0	17	AAR77971	Aar77971 H. influe
24	40	100.0	17	AAV51786	Aav51786 H. influe
25	40	100.0	17	AAW54130	Aaw54130 Polioviru

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Bagat, Minna, DL63

and non-typable strain PAKI2085. The transferrin receptor (TFR) operon

consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are

transcribed from a single promoter. H. influenzae TFR is iron- and/or

haem-regulated and a putative fur-binding site has been identified

upstream of tbp2. Antibodies blocking this binding site may prevent

bacterial growth. Fragments of the TFR (or its genes) are useful in

vaccines to provide protection against, e.g. bacterial meningitis. An

advantage of using the TFR is that it shares homology with TFR of other

H. influenzae strains including non-typable strains. According to the

CC specification the present sequence shows residues 231-238 of Tbp2 from the H. influenzae strain Eagan	SQ Sequence 7 AA;	Query Match Score 40; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 40; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	XX	XX
Query Match Score 40; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 LEGGFYGV 7 Db 1 LEGGFYGV 7	Qy 1 LEGGFYGV 7 Db 1 LEGGFYGV 7	Qy 1 LEGGFYGV 7 Db 1 LEGGFYGV 7
XX	XX	XX	XX
RESULT 3	AAY51767	RESULT 3	AAY51767
XX	XX	XX	XX
ID AAW46162 standard; protein; 7 AA.	ID AAY51767 standard; protein; 7 AA.	ID AAY51767 standard; protein; 7 AA.	ID AAY51767 standard; protein; 7 AA.
XX	XX	XX	XX
DB Predicted antigenic Tbp1 peptide TBP2-36.	DB H. influenzae antigenic Tbp2 peptide TBP2-36.	DB H. influenzae antigenic Tbp2 peptide TBP2-36.	DB H. influenzae antigenic Tbp2 peptide TBP2-36.
XX	XX	XX	XX
KW Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.	KW Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.	KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.	KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.
XX	XX	XX	XX
DT 05-MAY-1998 (first entry)	DT 13-JUN-2000 (first entry)	DT 13-JUN-2000 (first entry)	DT 13-JUN-2000 (first entry)
XX	XX	XX	XX
OS Synthetic.	OS Haemophilus influenzae.	OS Haemophilus influenzae.	OS Haemophilus influenzae.
XX	XX	XX	XX
PN WO9640929-A2.	PN US615688-A.	PN US615688-A.	PN US615688-A.
XX	XX	XX	XX
PD 19-DEC-1996.	PD 18-JAN-2000.	PD 18-JAN-2000.	PD 18-JAN-2000.
XX	XX	XX	XX
PP 07-JUN-1996;	PP 07-JUN-1995;	PP 07-JUN-1995;	PP 07-JUN-1995;
XX	XX	XX	XX
PR 07-JUN-1995;	PR 08-NOV-1993;	PR 08-NOV-1993;	PR 08-NOV-1993;
PR 17-JUN-1996;	PR 29-DEC-1993;	PR 29-DEC-1993;	PR 29-DEC-1993;
XX	XX	XX	XX
PA (CONN-) CONNAUGHT LAB LTD.			
XX	XX	XX	XX
PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;	PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;	PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;	PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
PI Murdin A, Klein M, Chong P;			
XX	XX	XX	XX
DR WPI: 1997-052329/05.	DR WPI: 1997-052329/05.	DR WPI: 1997-052329/05.	DR WPI: 1997-052329/05.
XX	XX	XX	XX
PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
XX	XX	XX	XX
PS Example 16: Page 71; 228pp; English.			
XX	XX	XX	XX
PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.	PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
XX	XX	XX	XX
PS AAAG6126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes	PS AAAG6126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes	PS AAAG6126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes	PS AAAG6126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes
XX	XX	XX	XX
SQ Sequence 7 AA;			

AAW54121	standard; peptide; 7 AA.	XX	10-DEC-1998.
XX		XX	ID 98WO-CR000544.
AC		PP 02-JUN-1998;	
DT	20-JUL-1998 (first entry)	XX	PR 03-JUN-1997;
XX	Tbp2 antigenic peptide TBP2-36.	PR 08-MAY-1998;	97US-00867941.
DB		XX	98US-00074658.
XX		(CONN-) CONNAUGHT LAB LTD.	
KW	tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;	XX	
KW	passive immunisation; transferin receptor operon.	PI Loosmore SM, Du R, Wang Q, Yang Y, Klein M;	
XX	Haemophilus influenzae.	XX	WPI; 1999-070266/06.
CS		DR XX	
XX		Lactoferrin receptor genes from Moraxella, especially M. catarrhalis -	
PN	US5708149-A.	XX	especially M. catarrhalis - useful to diagnose Moraxella infection e.g. to detect otitis media due to M. catarrhalis infection and to immunise against such infections.
XX		PT XX	
PP	08-NOV-1993; 93US-00148968.	CC This peptide is an epitope of Moraxella lactoferrin binding protein 2 (Lbp2, see AAW89413, AAW89417 and AAW89421) that is also found in Haemophilus influenzae and Neisseria meningitidis Tbp2. The invention provides immunogenic compositions, including vaccines, based upon expressed recombinant Moraxella Lbp1 and/or Lbp2 and/or ORF3 proteins (see AAW89413-21) for use in the prevention of diseases, such as otitis media, that are caused by Moraxella	
PD	29-DEC-1993; 93US-00175116.	CC	
13-JAN-1998.	08-NOV-1994; 94US-00337483.	CC	
XX		CC	
PP	07-JUN-1995; 95US-00487890.	PS Example 13; Page 52; 202pp; English.	
XX		XX	
PR	08-NOV-1993; 93US-00148968.	CC	
PR	29-DEC-1993; 93US-00175116.	CC	
XX	08-NOV-1994; 94US-00337483.	CC	
PA	(CONN-) CONNAUGHT LAB LTD.	CC	
XX		CC	
PY	Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;	XX	
PI	Murdin A, Schryvers A;	SQ Sequence 7 AA;	
DR	WPI; 1998-100410/09.	Query Match 100.0%; Score 40; DB 2; Length 7;	
XX		Best Local Similarity 100.0%; Pred. No. 1.8e+06;	
PR	Purification of recombinant Haemophilus transferrin-binding protein - by solubilising inclusion bodies separated from cell lysate.	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Db 1 LEGGIFYG 7	
PS	Example 16/17; Column 37-38; 261PP; English.	Qy 1 LEGGIFYG 7	
XX		Db 1 LEGGIFYG 7	
CC	Peptides AAW53086-W53100 and peptides AAW5100-W54122 are derived from the Tbp2 protein. The Tbp2 protein is one of two proteins with genes found on the transferrin operon. These peptides can be used along with the genes, DNA sequences and recombinant proteins for diagnosis, immunisation and the generation of diagnostic and immunological reagents.	RESULT 6 AAY80464	
CC	They can also be used to protect from bacteria that produce transferrin receptor protein	ID AAY80464 standard; peptide; 7 AA.	
CC		XX	
XX		AC AAY80464;	
XX		XX	
XX		DT 06-JUN-2000 (first entry)	
XX		XX	
XX		H. influenzae transferrin receptor Tbp1 epitope TBP2-36.	
DB		DB XX	
XX		Antibacterial; antiinflammatory; auditory; respiratory; antibody;	
XX		KW antiserum; transferrin receptor; immunogen; epitope; otitis media;	
XX		KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.	
XX		OS Haemophilus influenzae.	
XX		XX	
XX		US6008326-A.	
XX		PN	
XX		XX	
XX		PD 28-DEC-1999.	
XX		XX	
XX		PR 07-JUN-1995; 95US-00474671.	
XX		XX	
XX		PR 08-NOV-1993; 93US-00148968.	
XX		PR 29-DEC-1993; 93US-00175116.	
DB	21-JUN-1999 (first entry)	PR 08-NOV-1995; 95US-0037483.	
XX	Moraxella lactoferrin binding protein 2 (Lbp2) epitope.	XX	
XX		(CONN-) CONNAUGHT LAB LTD.	
KW	Lactoferrin receptor; lactoferrin binding protein; Lbp1; lbpA gene; infection; otitis media; sinusitis; conjunctivitis; pneumonia;	PA	
KW	bronchitis; tracheitis; emphysema; diagnosis; therapy; vaccine;	XX	
KW	Branhamella catarrhalis; epitope.	PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;	
XX		PI Murdin A, Schryvers A;	
XX		XX	
OS	Moraxella catarrhalis.	DR WPI; 2000-096387/08.	
PN		XX	
PN	W09855606-A2.		

PT influenzae, useful for treating otitis media, epiglottitis, pneumonia and tracheobronchitis.
 PT Disclosure; Col 39-40; 252pp; English.
 XX
 CC The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic fragments) from strains of Haemophilus influenzae. This sequence corresponds to an epitope from the H. influenzae transferrin receptor protein Tbp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used to detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbent assay (ELISA)) and hence diagnose infections.

XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 40; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGYG 7
 Db 1 LEGGYG 7

RESULT 7
 ID AAR77958 standard; peptide; 8 AA.
 XX
 AC AAR77958
 XX DT 09-OCT-1996 (first entry)
 XX DE Antigenic Tbp2 peptide TBP2-25.
 XX KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; non-typable strain; Haemophilus influenzae; meningitis.
 XX OS Synthetic.
 XX PN WO95133370-A1.
 XX PR 08-NOV-1993; 94WO-CA000615.
 XX PR 08-NOV-1993; 93US-00148968.
 XX PR 29-DEC-1993; 93US-00175116.
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX PD 18-MAY-1995.
 XX PI Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
 PI Yang Y, Murdin A, Klein M;
 DR WPI; 1995-194089/25.
 XX PS Example 16; Page 71; 228pp; English.

XX
 CC advantage of using the TFR is that it shares homology with TFR of other H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 231-238 of Tbp2 from the H. influenzae strain Bagan.
 CC Sequence 8 AA;
 SQ Query Match 100.0%; Score 40; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGYFG 7
 Db 1 LEGGYFG 7

RESULT 8
 ID AAW46151 standard; protein; 8 AA.
 XX AC AAW46151;
 XX DT 05-MAY-1998 (first entry)
 XX DE Predicted antigenic Tbp1 peptide TBP2-25.
 XX KW Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.
 XX KW
 XX OS Synthetic.
 OS Haemophilus influenzae.
 XX PN WO9640929-A2.
 XX PR 19-DEC-1996.
 XX PR 07-JUN-1996; 96WO-CA000399.
 XX PR 07-JUN-1995; 95US-00483577.
 XX PR 17-MAY-1996; 96US-00649518.
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loosmore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;
 PI Yang Y, Murdin AD, Klein M;
 DR WPI; 1997-052329/05.
 XX PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TFR antibodies.
 XX PS Example 16; Page 71; 228pp; English.
 XX CC AAW46126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 231-238. Iron is an essential nutrient for the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The CC transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the CC immunogenic truncated analogue can be used to induce protection against a CC disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen CC in immunoassays for the detection of Haemophilus transferrin receptor CC antibodies, while the nucleic acid molecule can be used as a CC hybridisation probe for the detection of other transferrin receptor genes CC

SQ	Sequence 8 AA;							
Query	Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Db	Score 40; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;	DB 2; Length 8;					
AAW54110	ID AAW54110 standard; peptide; 8 AA.	XX	XX	XX	XX	XX	XX	XX
AAW54110;	AC AAW54110;	XX	DT 20-JUL-1998 (First entry)	XX	XX	XX	XX	XX
Tbp2 antigenic peptide TBP2-25.	KW tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; transferrin receptor operon.	XX	XX	XX	XX	XX	XX	XX
Haemophilus influenzae.	OS Haemophilus influenzae.	XX	OS US5708149-A.	XX	PN PN	PD PD	PR PR	PR PR
AAW51756	ID AAY51756 standard; peptide; 8 AA.	XX	XX	XX	XX	XX	XX	XX
AAY51756;	AC AC	XX	DT 13-JUN-2000 (First entry)	XX	XX	XX	XX	XX
H. influenzae antigenic Tbp2 peptide TBP2-25.	DH H. influenzae antigenic Tbp2 peptide TBP2-25.	XX	XX	XX	XX	XX	XX	XX
Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.	KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine; diagnosis.	XX	XX	XX	XX	XX	XX	XX
Haemophilus influenzae.	OS OS Haemophilus influenzae.	XX	XX	XX	XX	XX	XX	XX
US6015688-A.	PN PN	XX	PA PA	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	XX	XX	XX	XX	XX	XX	XX	XX
18-JAN-2000.	PP PP	XX	07-JAN-1995; 95US-00483577.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	PD PD	XX	08-NOV-1993; 93US-00148968.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	PI PI	XX	29-DEC-1993; 93US-00175116.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	DR DR	XX	08-NOV-1994; 94US-00337483.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	WPI WPI	XX	WPI: 1997-052329/05.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	PT PT	XX	WPI: 1997-052329/05.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	PR PR	XX	WPI: 1997-052329/05.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	DR DR	XX	WPI: 1997-052329/05.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	PS PS	XX	Example 16; Col 39-40; 281pp; English.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae which has antibacterial activity. (I) are used for recombinant production of truncated Tbp, as probes and primers for detecting, and diagnosing infection by, Haemophilus, also for isolating similar sequences from other bacteria; as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g. Haemophilus, Neisseria or Branhamella. The truncated proteins are useful as immunogens (as above); for diagnosing infection (as antigens in immunoassays) and for raising antibodies, used for diagnosis of infections or for passive immunization. AAY51695-Y51767 represent H. influenzae transferrin receptor proteins Tbp1 and Tbp2 antigenic peptide fragments	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Sequence 8 AA;	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Db	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Score 40; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	DB 2; Length 8;	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiseraum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Haemophilus influenzae.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	RESULT 11 AAY80453 standard; peptide; 8 AA.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	ID AAY80453	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Db	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Score 40; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	DB 2; Length 8;	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiseraum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.	XX	XX	XX	XX	XX
CONNAUGHT LAB LTD.	CC CC	XX	Haemophilus influenzae.	XX	XX	XX	XX	XX

PN US6008326-A.
 XX PD 28-DEC-1999.
 XX PF 07-JUN-1995; 95US-00474671.
 XX PR 08-NOV-1993; 93US-0018968.
 PR 29-DEC-1993; 93US-00175116.
 PR 08-NOV-1995; 95US-0037483.
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
 Murdin A, Schryvers A;
 WPI; 2000-096387/08.
 XX PT Antibodies specific for transferrin receptor proteins of Haemophilus
 influenzae, useful for treating otitis media, epiglottitis, pneumonia and
 tracheobronchitis.
 XX Disclosure; Col 37-38; 252pp; English.
 XX The invention relates to novel antibodies (or monospecific antisera)
 CC specific for single transferrin receptor proteins (or immunogenic
 fragment) from strains of Haemophilus influenzae. This sequence
 CC corresponds to an epitope from the H. influenzae transferrin receptor
 protein Tbp2. The antibodies may be used for preventing and treating
 CC infections and disorders caused by H. influenzae, including bacterial
 CC meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.
 CC The antibodies may also be used to detect the presence of H. influenzae
 CC proteins in samples according to standard methodologies (e.g. enzyme
 linked immunosorbant assay (ELISA), and hence diagnose infections
 XX Sequence 8 AA;
 SQ Query Match 100.0%; Score 40; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGFYG 7
 Db 1 LEGGFYG 7
 XX RESULT 12
 ID AAR77974 standard; peptide; 15 AA.
 XX AC AAR77974;
 XX DT 09-OCT-1996 (first entry)
 XX DE H. influenzae Tbp2 epitope used to construct pT7TBP2D.
 XX KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; vector;
 KW non-typable strain; Haemophilus influenzae; meningitis; poliovirus.
 XX OS Synthetic.
 XX PN WO95133370-A1.
 PD 18-MAY-1995.
 XX PP 07-NOV-1994; 94WO-CA000616.
 XX PR 08-NOV-1993; 93US-00148968.
 PR 29-DEC-1993; 93US-00175116.
 PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S,
 PI Yang Y, Murdin A, Klein M, Chong P;
 XX DR WPI; 1995-194089/25.
 XX PT Nucleic acids encoding Haemophilus transferrin receptor - used to develop
 PT products for detection and in diagnosis, prevention and treatment of
 Haemophilus infection.
 XX PS Example 20; Fig 29; 231pp; English.
 XX CC The transferrin receptor (TFR) operon consists of two genes (Tbp1 and
 CC Tbp2) arranged in tandem and are transcribed from a single
 CC promoter. Fragments of the Tfr (or its genes) are useful in vaccines to
 provide protection against, e.g. bacterial meningitis. A cDNA clone
 (AAQ94452) of the Poliovirus type 1, Mahoney strain (PV1-M) genome was
 CC cut with SauI and HindIII excising a fragment contg. bases 2734-2786
 CC which encodes AAR7790. (Residues 1095 is amino acid 95 of capsid protein
 CC VP1). New hybrid cDNA clones encoding both Poliovirus and transferrin
 CC receptor amino acid sequences were constructed by replacing the excised
 CC fragment with oligonucleotides encoding amino acids from H. influenzae
 CC Tbp2 (AAR77971-74). Transfection of Vero cells with the hybrid RNA
 CC transcripts produced 4 viable hybrid viruses, designated PV1TBP2A,
 CC PV1TBP2B, PV1TBP2C and PV1TBP2D.
 XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 40; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEGGFYG 7
 Db 7 LEGGFYG 13
 XX RESULT 13
 AAQ51789
 ID AAQ51789 standard; protein; 15 AA.
 XX AC AAQ51789;
 XX DT 13-JUN-2000 (first entry)
 DE H. influenzae transferrin receptor protein fragment #5.
 XX KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
 KW diagnosis.
 XX OS Haemophilus influenzae.
 XX PN US6015688-A.
 XX PD 18-JAN-2000.
 XX PF 07-JUN-1995; 95US-00483577.
 XX PR 08-NOV-1993; 93US-00148968.
 PR 29-DEC-1993; 93US-00175116.
 PR 08-NOV-1994; 94US-001337483.
 PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
 PI Murdin A, Klein M, Chong P;
 XX DR WPI; 1997-052329/05.
 XX PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
 PT to induce protection against disease caused by transferrin producing
 PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.
 XX PS Disclosure; Col 235-236; 281pp; English.
 XX CC This invention describes a novel isolated and purified nucleic acid (I)

encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae which has antibacterial activity. (I) are used for recombinant production of truncated Tbp, as probes and primers for detecting, and diagnosing infection by, Haemophilus, also for isolating similar sequences from other bacteria, as immunogens for vaccinating against infections caused by bacteria that produce transferrin receptors, e.g. Haemophilus, Neisseria or Branhamella. The truncated proteins are useful as immunogens (as above), for diagnosing infection (as antigens in immunoassays) and for raising antibodies, used for diagnosis of infections or for passive immunization. This sequence represents a fragment of a H. influenzae transferrin receptor protein.

Sequence 15 AA:

Query Match 100.0%; Score 40; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sq

Qy 1 LEGGFYVG 7
 Db 7 LEGGFYVG 13

RESULT 14

AAW54133

ID AAW54133 standard; peptide; 15 AA.

XX AC AAW54133;

XX DT 20-JUL-1998 (first entry)

XX DB Poliovirus Plasmid pV1TB2D encoded peptide.

XX KW Transferrin receptor; antigen; virus; prevention; pathogens.

XX OS Synthetic.

OS Poliovirus

OS Haemophilus influenzae.

XX PN US5708149-A.

XX PD 13-JAN-1998.

XX PP 07-JUN-1995; 95US-00487890.

XX PR 08-NOV-1993; 93US-00148968.

PR 29-DEC-1993; 93US-00175116.

PR 08-NOV-1994; 94US-00337483.

PA (CONN-) CONNAUGHT LAB LTD.

XX PI Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;

PI Murdin A, Schryvers A;

DR WPI: 1998-100410/09.

XX Purification of recombinant Haemophilus transferrin-binding protein - by PT solubilising inclusion bodies separated from cell lysate.

XX PS Example 20; Fig 29; 261PP; English.

XX Peptides (AAW54129-W54133) are encoded by plasmids encoding a chimeric poliovirus expressing an epitope LEGGFYVG. The epitope is derived from the transferrin receptor protein that is conserved among bacteria that produce transferrin receptor protein. These viruses expressed the epitope sequence in an antigenically recognisable form. Viruses based upon expressed recombinant transferrin receptor protein can be used for the prevention of diseases caused by bacterial pathogens that produce transferrin receptor

XX Sequence 15 AA;

CC Query Match 100.0%; Score 40; DB 3; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 1.9;

CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sq Qy 1 LEGGFYVG 7

Db 7 LEGGFYVG 13

Query Match 100.0%; Score 40; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sq

Qy 1 LEGGFYVG 7
 Db 7 LEGGFYVG 13

RESULT 15

AAW80391

ID AAY80391 standard; protein; 15 AA.

XX AC AAY80391;

XX XX 06-JUN-2000 (first entry)

XX DB H. influenzae transferrin receptor protein epitope TB2D.

XX KW Antibacterial; antiinflammatory; auditory; respiratory; antibody; primer;

KW antisera; transferrin receptor; immunogen; epitope; otitis media; PCR;

KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ss.

XX OS Haemophilus influenzae.

XX PN US6008326-A.

XX XX 28-DEC-1999.

XX PD 07-JUN-1995; 95US-00474671.

XX PR 08-NOV-1993; 93US-00148968.

PR 29-DEC-1993; 93US-00175116.

PR 08-NOV-1995; 95US-00337483.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;

PI Murdin A, Schryvers A;

XX DR WPI: 2000-096387/08.

XX PT Antibodies specific for transferrin receptor epitope of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia and tracheobronchitis.

XX PS Example 20; Fig 29; 252PP; English.

XX CC The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic fragment) from strains of Haemophilus influenzae. The antibodies can be generated by expressing transferrin receptor epitope on the surface of a vector protein. In an example, the vector is poliovirus and the epitopes are inserted into the capsid protein VP1. This sequence corresponds to the transferrin receptor epitope TB2D which is used to replace amino acids 95-102 of the poliovirus VP1 capsid protein (AAW80387). The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used to detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbent assay (ELISA)) and hence diagnose infections

XX SQ Sequence 15 AA;

CC Query Match 100.0%; Score 40; DB 3; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 1.9;

CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sq Qy 1 LEGGFYVG 7

Db 7 LEGGFYVG 13

Search completed: November 9, 2005, 19:22:43
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